FIG. 1-1

```
        10         20         30         40         50         60         70
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GACGGATCGG GAGATCTCCC GATCCCCTAT GGTCGACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT
        80         90        100        110        120        130        140
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA
       150        160        170        180        190        200        210
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG
       220        230        240        250        260        270        280
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ATGTACGGGC CAGATATACG CGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC
       290        300        310        320        330        340        350
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ATTAGTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG
       360        370        380        390        400        410        420
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC
       430        440        450        460        470        480        490
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ATTGACGTCA ATGGGTGGAC TATTTACGGT AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC
       500        510        520        530        540        550        560
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AAGTACGCCC CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA
       570        580        590        600        610        620        630
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG CGGTTTTGGC
       640        650        660        670        680        690        700
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AGTACATCAA TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
       710        720        730        740        750        760        770
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG
       780        790        800        810        820        830        840
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA
       850        860        870        880        890        900        910
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CTGCTTAACT GGCTTATCGA AATTAATACG ACTCACTATA GGGAGACCCA AGCTTCGCAG AATTCCTGCG
       920        930        940        950        960        970        980
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GCTGCTACAG TGTGTCCAGC GTCCTGCCTG GCTGTGCTGA GCGCTGGAAC AGTGGCGCAT CATTCAAGTG
       990       1000       1010       1020       1030       1040       1050
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CACAGTTACC CATCCTGAGT CTGGCACCTT AACTGGCACA ATTGCCAAAG TCACAGGTGA GCTCAGATGC
      1060       1070       1080       1090       1100       1110       1120
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ATACCAGGAC ATTGTATGAC GTTCCCTGCT CACATGCCTG CTTTCTTCCT ATAATACAGA TGCTCAACTA
      1130       1140       1150       1160       1170       1180       1190
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ACTGCTCATG TCCTTATATC ACAGAGGGAA ATTGGAGCTA TCTGAGGAAC TGCCCAGAAG GGAAGGGCAG
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FIG. 1-2

```
      1200       1210       1220       1230       1240       1250       1260
    *    *     *    *     *    *     *    *     *    *     *    *     *    *
AGGGGTCTTG CTCTCCTTGT CTGAGCCATA ACTCTTCTTT CTACCTTCCA GTGAACACCT TCCCACCCCA
      1270       1280       1290       1300       1310       1320       1330
    *    *     *    *     *    *     *    *     *    *     *    *     *    *
GGTCCACCTG CTACCGCCGC CGTCGGAGGA GCTGGCCCTG AATGAGCTCT TGTCCCTGAC ATGCCTGGTG
      1340       1350       1360       1370       1380       1390       1400
    *    *     *    *     *    *     *    *     *    *     *    *     *    *
CGAGCTTTCA ACCCTAAAGA AGTGCTGGTG CGATGGCTGC ATGGAAATGA GGAGCTGTCC CCAGAAAGCT
      1410       1420       1430       1440       1450       1460       1470
    *    *     *    *     *    *     *    *     *    *     *    *     *    *
ACCTAGTGTT TGAGCCCCTA AAGGAGCCAG GCGAGGGAGC CACCACCTAC CTGGTGACAA GCGTGTTGCG
      1480       1490       1500       1510       1520       1530       1540
    *    *     *    *     *    *     *    *     *    *     *    *     *    *
TGTATCAGCT GAAAGCTTGA TATCGAATTC CGGAGGCGGA ACCGGCAGTG CAGCCCGAAG CCCCGCAGTC
      1550       1560       1570       1580       1590
    *    *     *    *     *    *     *    *     *    *     *
CCCGAGCACG CGTGGCC ATG CGT CCC CTG CGC CCC CGC GCC GCG CTG CTG GCG CTC CTG
                   Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu
1600       1610       1620       1630       1640       1650
  *    *     *    *     *    *     *    *     *    *     *    *
GCC TCG CTC CTG GCC GCG CCC CCG GTG GCC CCG GCC GAG GCC CCG CAC CTG GTG CAT
Ala Ser Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val His
 1660       1670       1680       1690       1700       1710
    *    *     *    *     *    *     *    *     *    *     *
GTG GAC GCG GCC CGC GCG CTG TGG CCC CTG CGG CGC TTC TGG AGG AGC ACA GGC TTC
Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe
     1720       1730       1740       1750       1760       1770
  *    *     *    *     *    *     *    *     *    *     *    *
TGC CCC CCG CTG CCA CAC AGC CAG GCT GAC CAG TAC GTC CTC AGC TGG GAC CAG CAG
Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln
        1780       1790       1800       1810       1820
     *    *     *    *     *    *     *    *     *    *     *
CTC AAC CTC GCC TAT GTG GGC GCC GTC CCT CAC CGC GGC ATC AAG CAG GTC CGG ACC
Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr
1830       1840       1850       1860       1870       1880
  *    *     *    *     *    *     *    *     *    *     *    *
CAC TGG CTG CTG GAG CTT GTC ACC ACC AGG GGG TCC ACT GGA CGG GGC CTG AGC TAC
His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr
   1890       1900       1910       1920       1930       1940
*    *     *    *     *    *     *    *     *    *     *    *
AAC TTC ACC CAC CTG GAC GGG TAC CTG GAC CTT CTC AGG GAG AAC CAG CTC CTC CCA
Asn Phe Thr His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
      1950       1960       1970       1980       1990
    *    *     *    *     *    *     *    *     *    *     *
GGG TTT GAG CTG ATG GGC AGC GCC TCG GGC CAC TTC ACT GAC TTT GAG GAC AAG CAG
Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln
```

FIG. 1-3

```
2000          2010          2020          2030          2040          2050
   *     *     *     *     *     *     *     *     *     *     *     *
  CAG GTG TTT GAG TGG AAG GAC TTG GTC TCC AGC CTG GCC AGG AGA TAC ATC GGT AGG
  Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg
    2060          2070          2080          2090          2100          2110
       *     *     *     *     *     *     *     *     *     *     *
  TAC GGA CTG GCG CAT GTT TCC AAG TGG AAC TTC GAG ACG TGG AAT GAG CCA GAC CAC
  Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His
         2120          2130          2140          2150          2160
     *     *     *     *     *     *     *     *     *     *     *
  CAC GAC TTT GAC AAC GTC TCC ATG ACC ATG CAA GGC TTC CTG AAC TAC TAC GAT GCC
  His Asp Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala
2170          2180          2190          2200          2210          2220
  *     *     *     *     *     *     *     *     *     *     *     *
  TGC TCG GAG GGT CTG CGC GCC GCC AGC CCC GCC CTG CGG CTG GGA GGC CCC GGC GAC
  Cys Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp
   2230          2240          2250          2260          2270          2280
      *     *     *     *     *     *     *     *     *     *     *
  TCC TTC CAC ACC CCA CCG CGA TCC CCG CTG AGC TGG GGC CTC CTG CGC CAC TGC CAC
  Ser Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His
       2290          2300          2310          2320          2330          2340
    *     *     *     *     *     *     *     *     *     *     *     *
  GAC GGT ACC AAC TTC TTC ACT GGG GAG GCG GGC GTG CGG CTG GAC TAC ATC TCC CTC
  Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu
            2350          2360          2370          2380          2390
       *     *     *     *     *     *     *     *     *     *     *
  CAC AGG AAG GGT GCG CGC AGC TCC ATC TCC ATC CTG GAG CAG GAG AAG GTC GTC GCG
  His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala
2400          2410          2420          2430          2440          2450
  *     *     *     *     *     *     *     *     *     *     *
  CAG CAG ATC CGG CAG CTC TTC CCC AAG TTC GCG GAC ACC CCC ATT TAC AAC GAC GAG
  Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu
     2460          2470          2480          2490          2500          2510
  *     *     *     *     *     *     *     *     *     *     *     *
  GCG GAC CCG CTG GTG GGC TGG TCC CTG CCA CAG CCG TGG AGG GCG GAC GTG ACC TAC
  Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr
         2520          2530          2540          2550          2560
      *     *     *     *     *     *     *     *     *     *     *
  GCG GCC ATG GTG GTG AAG GTC ATC GCG CAG CAT CAG AAC CTG CTA CTG GCC AAC ACC
  Ala Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr
2570          2580          2590          2600          2610          2620
  *     *     *     *     *     *     *     *     *     *     *     *
  ACC TCC GCC TTC CCC TAC GCG CTC CTG AGC AAC GAC AAT GCC TTC CTG AGC TAC CAC
  Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His
    2630          2640          2650          2660          2670          2680
       *     *     *     *     *     *     *     *     *     *     *
  CCG CAC CCC TTC GCG CAG CGC ACG CTC ACC GCG CGC TTC CAG GTC AAC AAC ACC CGC
  Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg
```

FIG. 1-4

```
        2690         2700         2710         2720         2730
     *    *    *    *    *    *    *    *    *    *    *
   CCG CCG CAC GTG CAG CTG TTG CGC AAG CCG GTG CTC ACG GCC ATG GGG CTG CTG GCG
   Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala
2740         2750         2760         2770         2780         2790
   *    *    *    *    *    *    *    *    *    *    *    *    *    *    *
   CTG CTG GAT GAG GAG CAG CTC TGG GCC GAA GTG TCG CAG GCC GGG ACC GTC CTG GAC
   Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp
    2800         2810         2820         2830         2840         2850
      *    *    *    *    *    *    *    *    *    *    *    *    *    *
   AGC AAC CAC ACG GTG GGC GTC CTG GCC AGC GCC CAC CGC CCC CAG GGC CCG GCC GAC
   Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
        2860         2870         2880         2890         2900         2910
    *    *    *    *    *    *    *    *    *    *    *    *    *    *
   GCC TGG CGC GCC GCG GTG CTG ATC TAC GCG AGC GAC GAC ACC CGC GCC CAC CCC AAC
   Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn
           2920         2930         2940         2950         2960
       *    *    *    *    *    *    *    *    *    *    *    *    *
   CGC AGC GTC GCG GTG ACC CTG CGG CTG CGC GGG GTG CCC CCC GGC CCG GGC CTG GTC
   Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val
2970         2980         2990         3000         3010         3020
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
   TAC GTC ACG CGC TAC CTG GAC AAC GGG CTC TGC AGC CCC GAC GGC GAG TGG CGG CGC
   Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg Arg
      3030         3040         3050         3060         3070         3080
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
   CTG GGC CGG CCC GTC TTC CCC ACG GCA GAG CAG TTC CGG CGC ATG CGC GCG GCT GAG
   Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu
          3090         3100         3110         3120         3130
       *    *    *    *    *    *    *    *    *    *    *    *    *
   GAC CCG GTG GCC GCG GCG CCC CGC CCC TTA CCC GCC GGC GGC CGC CTG ACC CTG CGC
   Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg
3140         3150         3160         3170         3180         3190
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
   CCC GCG CTG CGG CTG CCG TCG CTT TTG CTG GTG CAC GTG TGT GCG CGC CCC GAG AAG
   Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys
     3200         3210         3220         3230         3240         3250
       *    *    *    *    *    *    *    *    *    *    *    *    *
   CCG CCC GGG CAG GTC ACG CGG CTC CGC GCC CTG CCC CTG ACC CAA GGG CAG CTG GTT
   Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln Leu Val
         3260         3270         3280         3290         3300
    *    *    *    *    *    *    *    *    *    *    *    *    *
   CTG GTC TGG TCG GAT GAA CAC GTG GGC TCC AAG TGC CTG TGG ACA TAC GAG ATC CAG
   Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr Tyr Glu Ile Gln
3310         3320         3330         3340         3350         3360
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
   TTC TCT CAG GAC GGT AAG GCG TAC ACC CCG GTC AGC AGG AAG CCA TCG ACC TTC AAC
   Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn
```

FIG. 1-5

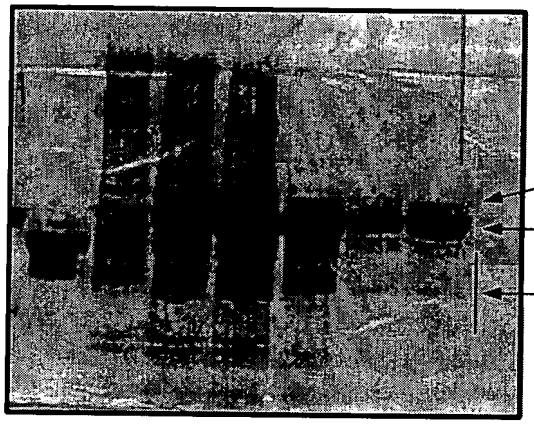
```
 3370         3380         3390         3400         3410         3420
    *    *    *    *    *    *    *    *    *    *    *    *
CTC TTT GTG TTC AGC CCA GAC ACA GGT GCT GTC TCT GGC TCC TAC CGA GTT CGA GCC
Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala
     3430         3440         3450         3460         3470         3480
 *    *    *    *    *    *    *    *    *    *    *    *    *    *
CTG GAC TAC TGG GCC CGA CCA GGC CCC TTC TCG GAC CCT GTG CCG TAC CTG GAG GTC
Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val
        3490         3500         3510         3520         3530         3540
    *    *    *    *    *    *    *    *    *    *    *    *    *    *
CCT GTG CCA AGA GGG CCC CCA TCC CCG GGC AAT CCA TGAG CCTGTGCTGA GCCCCAGTGG
Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
      3550         3560         3570         3580         3590         3600         3610
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
GTTGCACCTC CACCGGCAGT CAGCGAGCTG GGGCTGCACT GTGCCCATGC TGCCCTCCCA TCACCCCCTT
      3620         3630         3640         3650         3660         3670         3680
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
TGCAATATAT TTTTATATTT TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
      3690         3700         3710         3720         3730         3740         3750
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
AAAAAAAAAA AAAAAAAAAG AATTCCTGCA GCCCGGGGGA TCCACTAGTT CTAGAGGGCC CGTTTAAACC
      3760         3770         3780         3790         3800         3810         3820
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT
      3830         3840         3850         3860         3870         3880         3890
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
TGACCCTGGA AGGTGCCACT CCCACTGTCC TTTCCTAATA AAATGAGGAA ATTGCATCGC ATTGTCTGAG
      3900         3910         3920         3930         3940         3950         3960
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
TAGGTGTCAT TCTATTCTGG GGGGTGGGGT GGGGCAGGAC AGCAAGGGGG AGGATTGGGA AGACAATAGC
      3970         3980         3990         4000         4010         4020         4030
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
AGGCATGCTG GGGATGCGGT GGGCTCTATG GCTTCTGAGG CGGAAAGAAC CAGCTGGGGC TCGAGAGCTT
      4040         4050         4060         4070         4080         4090         4100
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
GGCGTAATCA TGGTCATAGC TGTTTCCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA CAACATACGA
      4110         4120         4130         4140         4150         4160         4170
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
GCCGGAAGCA TAAAGTGTAA AGCCTGGGGT GCCTAATGAG TGAGCTAACT CACATTAATT GCGTTGCGCT
      4180         4190         4200         4210         4220         4230         4240
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
CACTGCCCGC TTTCCAGTCG GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG
      4250         4260         4270         4280         4290         4300         4310
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
AGGCGGTTTG CGTATTGGGC GCTCTTCCGC TTCCTCGCTC ACTGACTCGC TGCGCTCGGT CGTTCGGCTG
      4320         4330         4340         4350         4360         4370         4380
   *    *    *    *    *    *    *    *    *    *    *    *    *    *
CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA
```

FIG. 1-6

```
      4390       4400       4410       4420       4430       4440       4450
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
AGAACATGTG AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTTCCA
      4460       4470       4480       4490       4500       4510       4520
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA
      4530       4540       4550       4560       4570       4580       4590
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA
      4600       4610       4620       4630       4640       4650       4660
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAA TGCTCACGCT GTAGGTATCT
      4670       4680       4690       4700       4710       4720       4730
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC
      4740       4750       4760       4770       4780       4790       4800
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
GCCTTATCCG GTAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGCCACTG GCAGCAGCCA
      4810       4820       4830       4840       4850       4860       4870
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA
      4880       4890       4900       4910       4920       4930       4940
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
CGGCTACACT AGAAGGACAG TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT
      4950       4960       4970       4980       4990       5000       5010
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTTTGCAAG CAGCAGATTA
      5020       5030       5040       5050       5060       5070       5080
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA
      5090       5100       5110       5120       5130       5140       5150
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
AAACTCACGT TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTAAATTAA
      5160       5170       5180       5190       5200       5210       5220
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA CTTGGTCTGA CAGTTACCAA TGCTTAATCA
      5230       5240       5250       5260       5270       5280       5290
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT
      5300       5310       5320       5330       5340       5350       5360
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
AACTACGATA CGGGAGGGCT TACCATCTGG CCCCAGTGCT GCAATGATAC CGCGAGACCC ACGCTCACCG
      5370       5380       5390       5400       5410       5420       5430
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
GCTCCAGATT TATCAGCAAT AAACCAGCCA GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT
      5440       5450       5460       5470       5480       5490       5500
       *  *       *  *       *  *       *  *       *  *       *  *       *  *
CCGCCTCCAT CCAGTCTATT AATTGTTGCC GGGAAGCTAG AGTAAGTAGT TCGCCAGTTA ATAGTTTGCG
```

FIG. 1-7

```
      5510        5520        5530        5540        5550        5560        5570
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
CAACGTTGTT GCCATTGCTA CAGGCATCGT GGTGTCACGC TCGTCGTTTG GTATGGCTTC ATTCAGCTCC
      5580        5590        5600        5610        5620        5630        5640
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
GGTTCCCAAC GATCAAGGCG AGTTACATGA TCCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC
      5650        5660        5670        5680        5690        5700        5710
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
CTCCGATCGT TGTCAGAAGT AAGTTGGCCG CAGTGTTATC ACTCATGGTT ATGGCAGCAC TGCATAATTC
      5720        5730        5740        5750        5760        5770        5780
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
TCTTACTGTC ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA
      5790        5800        5810        5820        5830        5840        5850
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
TAGTGTATGC GGCGACCGAG TTGCTCTTGC CCGGCGTCAA TACGGGATAA TACCGCGCCA CATAGCAGAA
      5860        5870        5880        5890        5900        5910        5920
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG AAAACTCTCA AGGATCTTAC CGCTGTTGAG
      5930        5940        5950        5960        5970        5980        5990
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTCAC CAGCGTTTCT
      6000        6010        6020        6030        6040        6050        6060
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAAGG GAATAAGGGC GACACGGAAA TGTTGAATAC
      6070        6080        6090        6100        6110        6120        6130
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
TCATACTCTT CCTTTTTCAA TATTATTGAA GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT
      6140        6150        6160        6170        6180        6190        6200
    *   *     *   *     *   *     *   *     *   *     *   *     *   *     *   *
TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCCGCGC ACATTTCCCC GAAAAGTGCC ACCTGACGTC
```



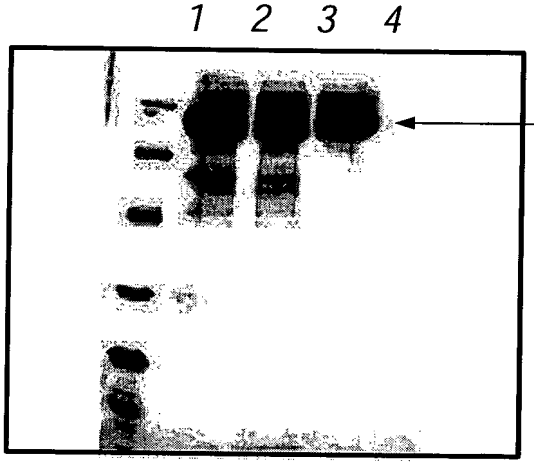


FIG. 2

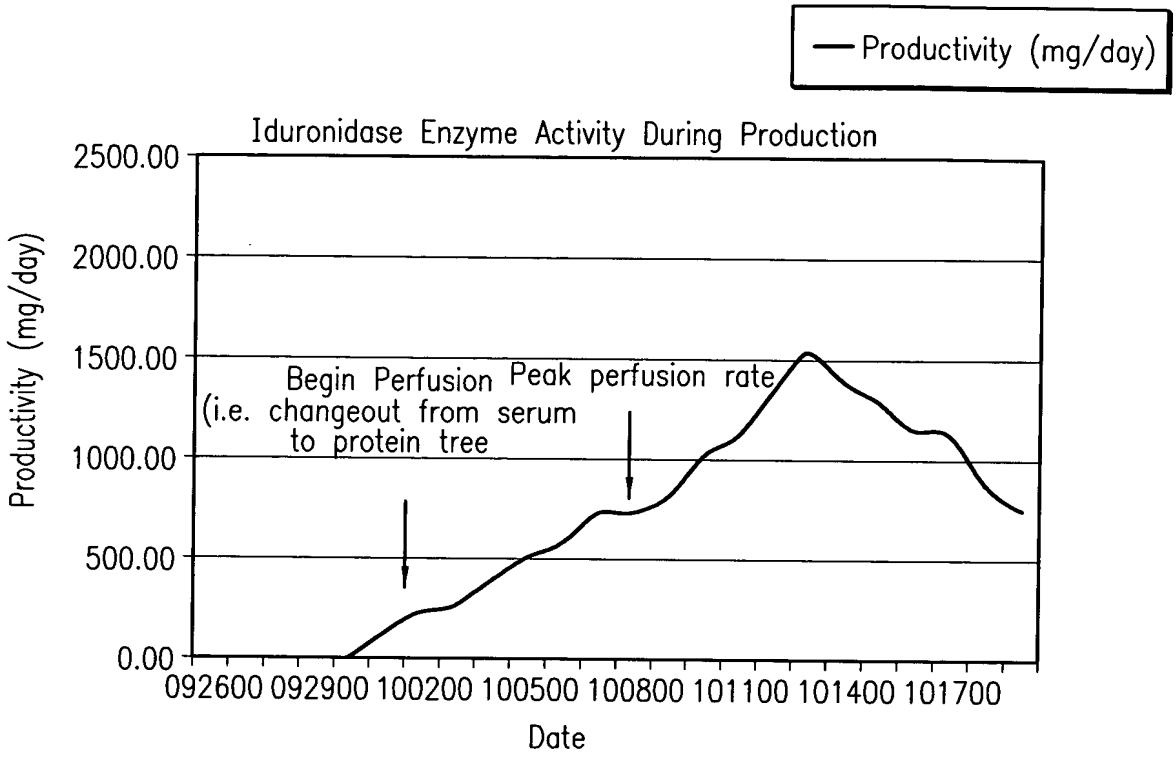


FIG. 3A

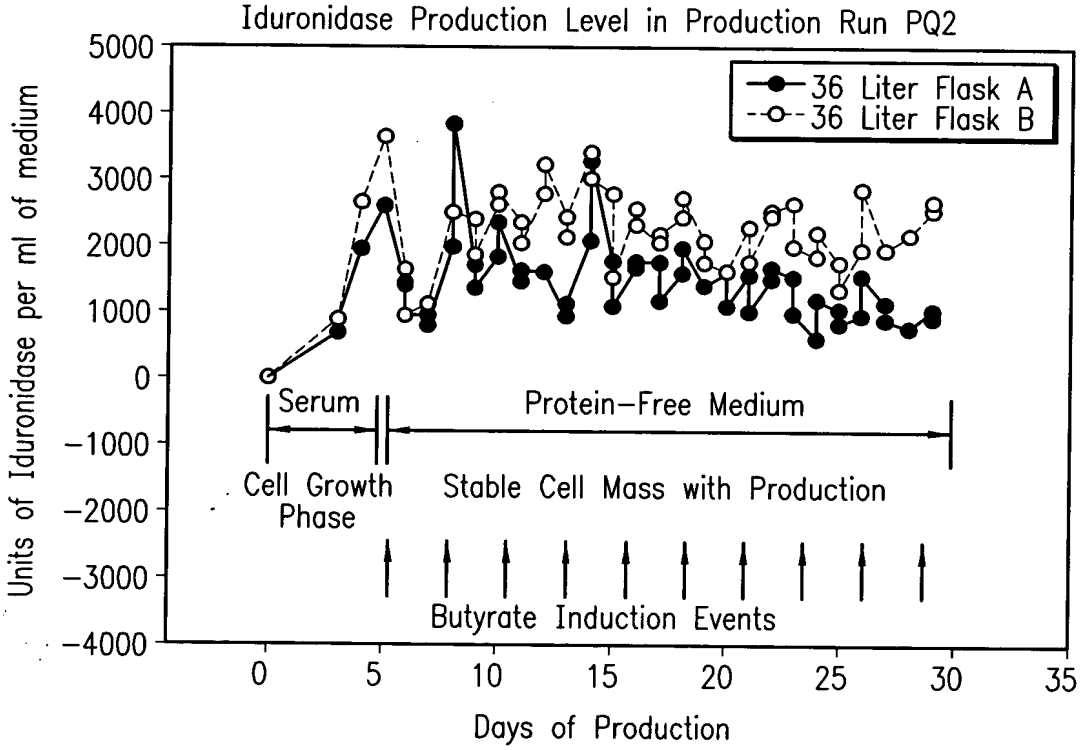
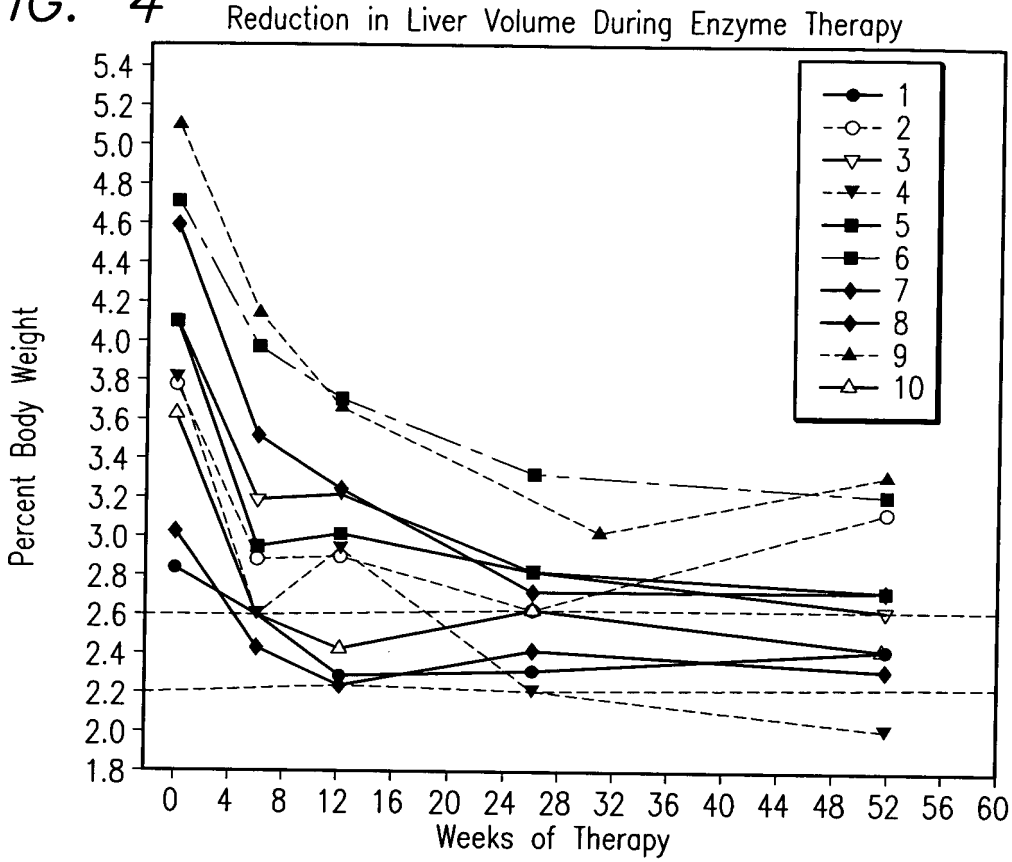


FIG. 3B

FIG. 4



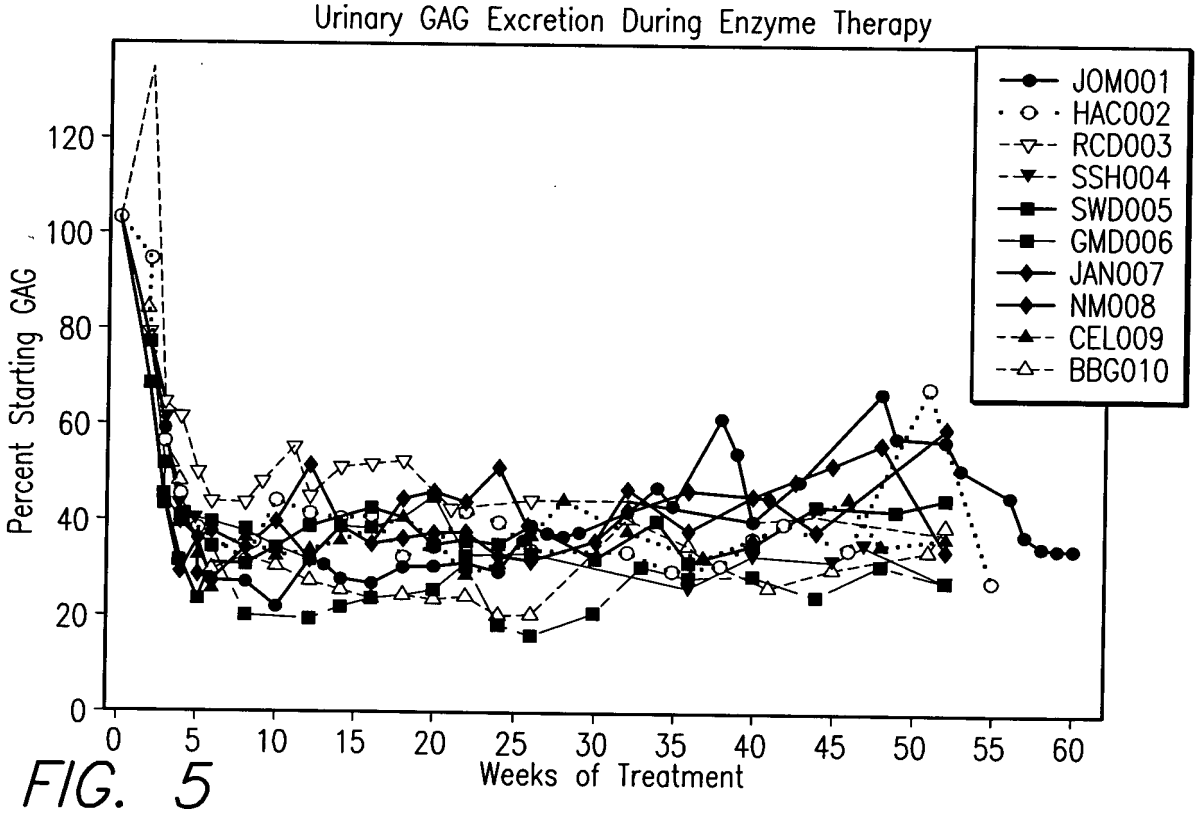
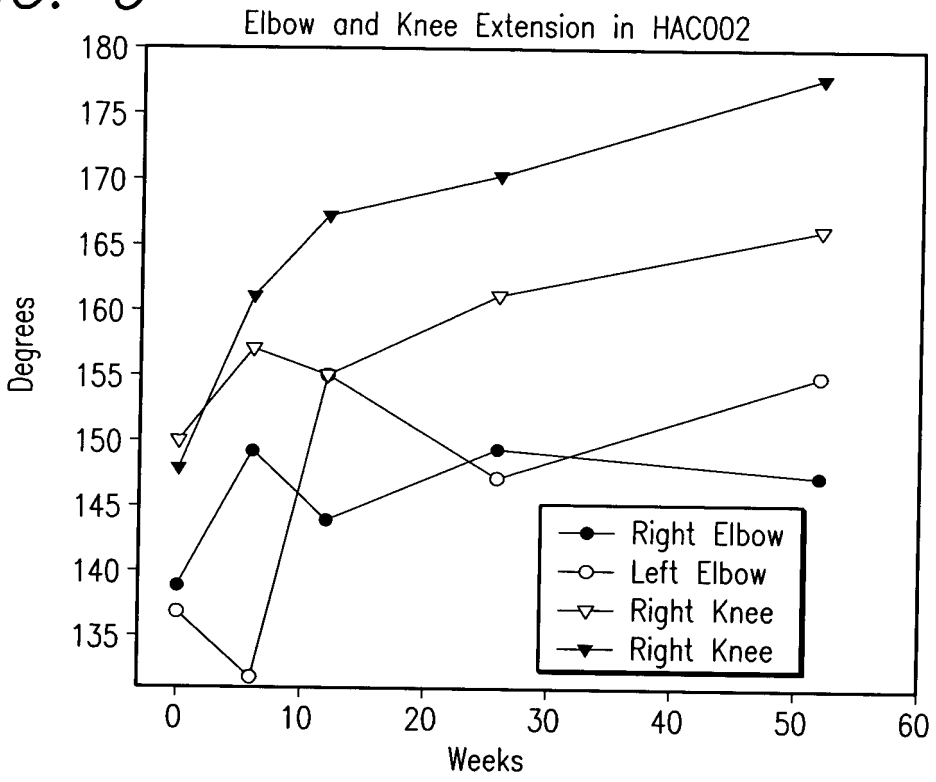


FIG. 5

FIG. 6



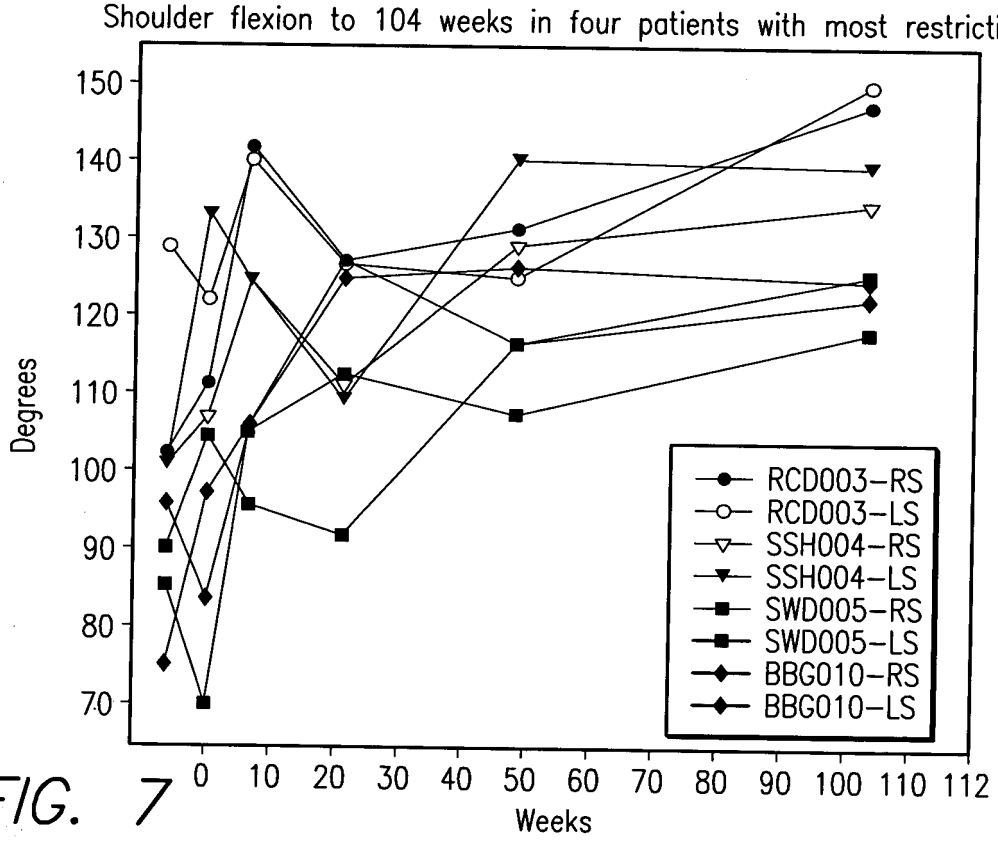


FIG. 7

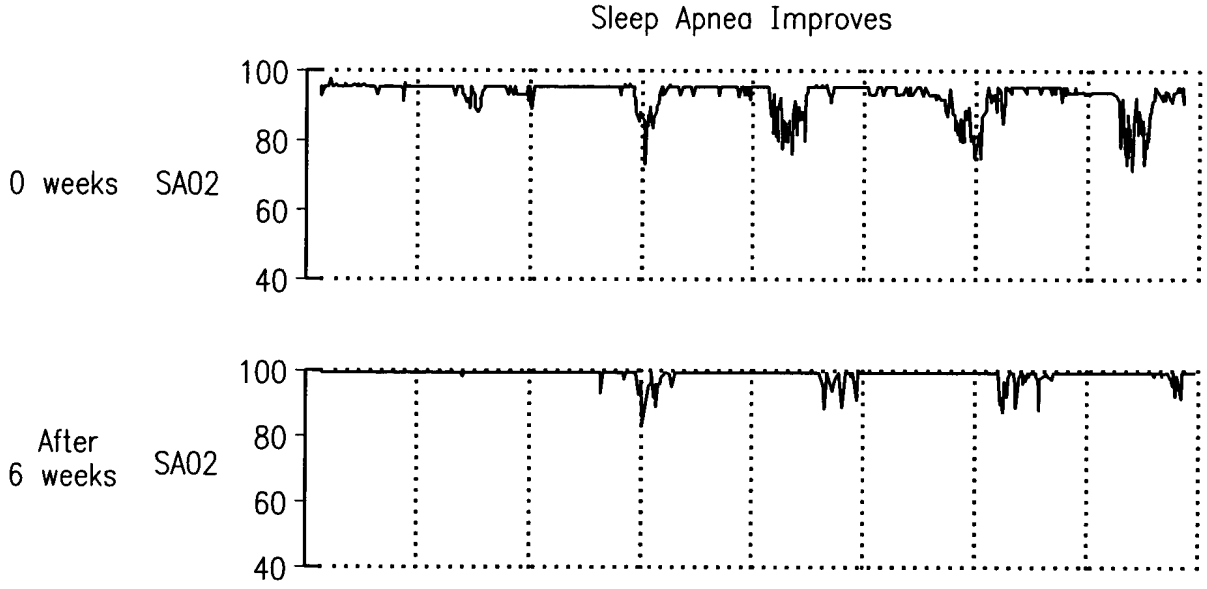


FIG. 8

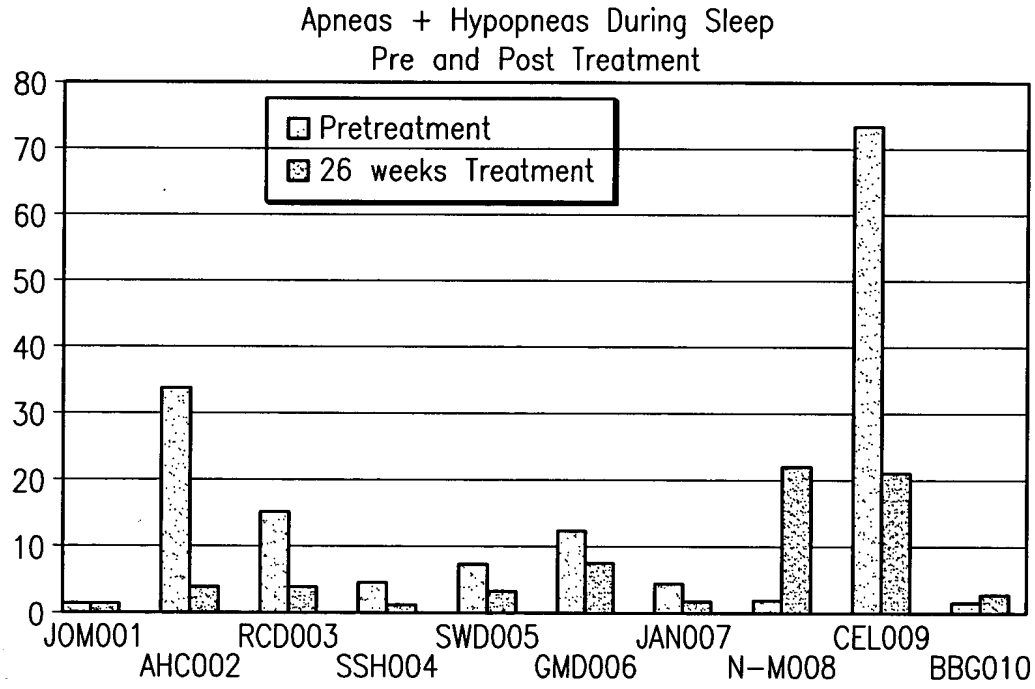


FIG. 9

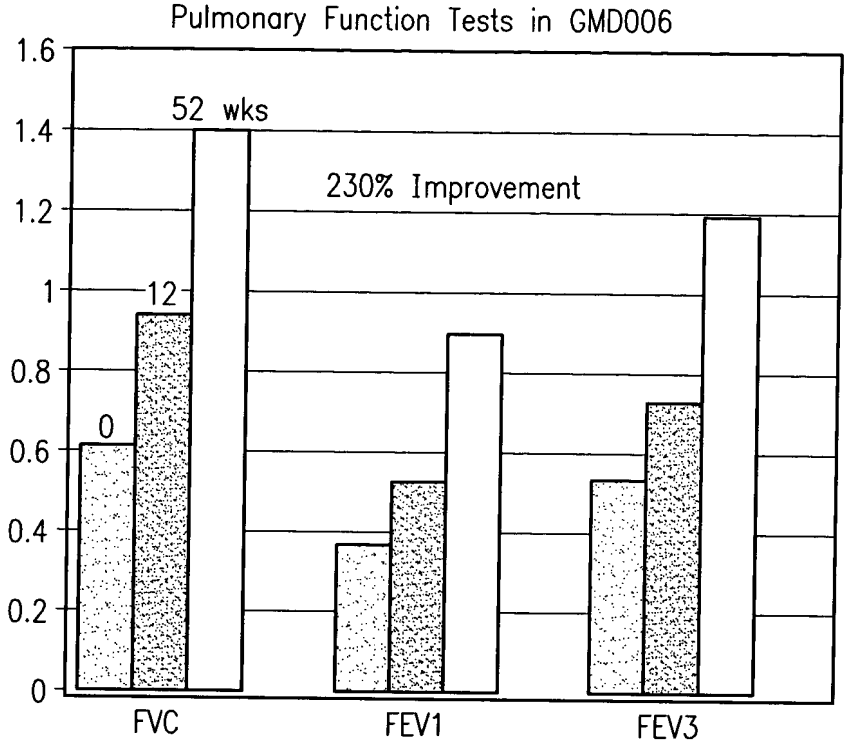


FIG. 10

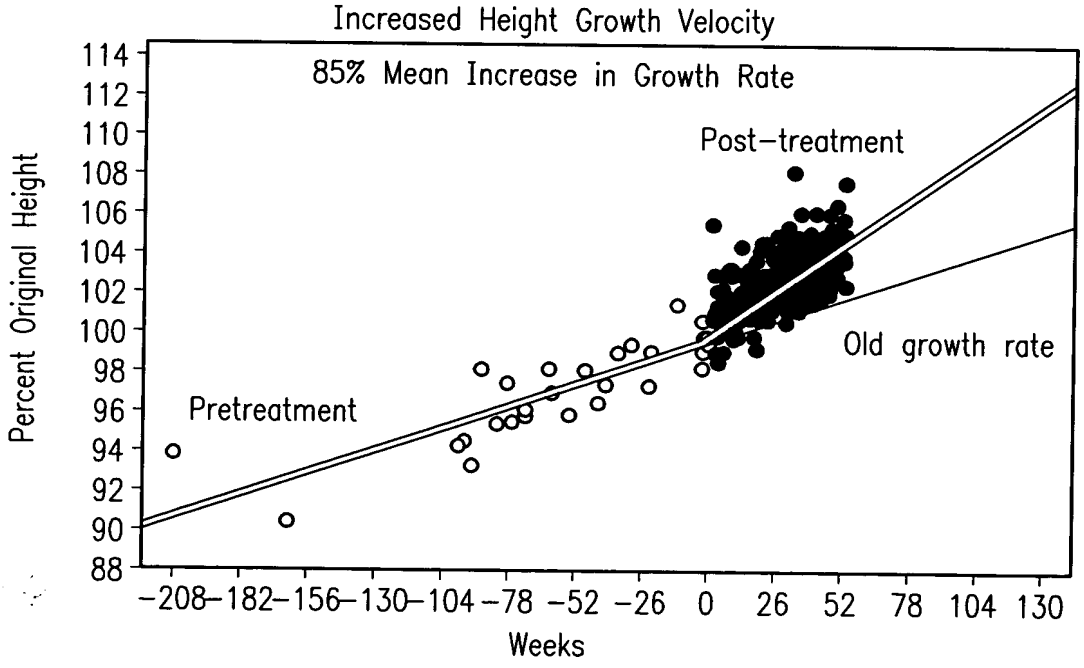


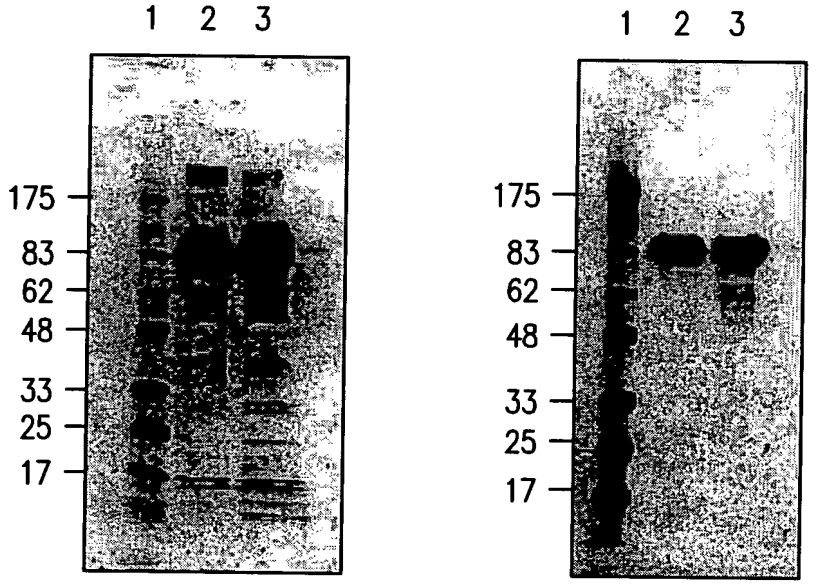
FIG. 11

FIG. 12

Chinese Hamster Ovary Host Protein Contamination by ELISA Assay

SOURCE AND BATCH NUMBER	CHOP PROTEIN CONTAMINATION (microgram per milligram)	PERCENT CHOP CONTAMINATION	PURITY OF THE ENZYME FROM CHOP
Prior Process (Carson/REI)			
C9002	14	1.4%	98.6%
C9003	24	2.4%	97.6%
C9004	16	1.6%	98.4%
New Process (Galli)			
P1003	<1.3	<0.13%	>99.9%
P1006	1.2	0.12%	99.9%
P1007	<0.6	<0.06%	>99.9%
P1008	<0.67	<0.067%	>99.9%

Comparison of Galli and Carson Material



anti-IDU Western blot 1:50,000

SDS-PAGE silver stain

1 Marker
2 Galli Referenced-0201
3 Carson C9002
5μg/lane

FIG. 13